FIG. 1

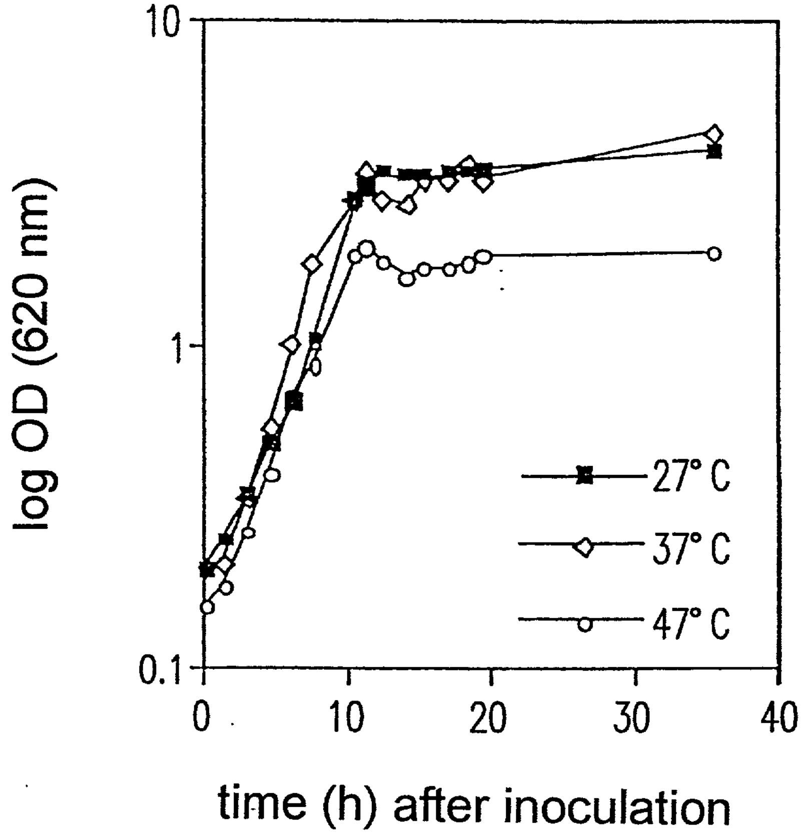
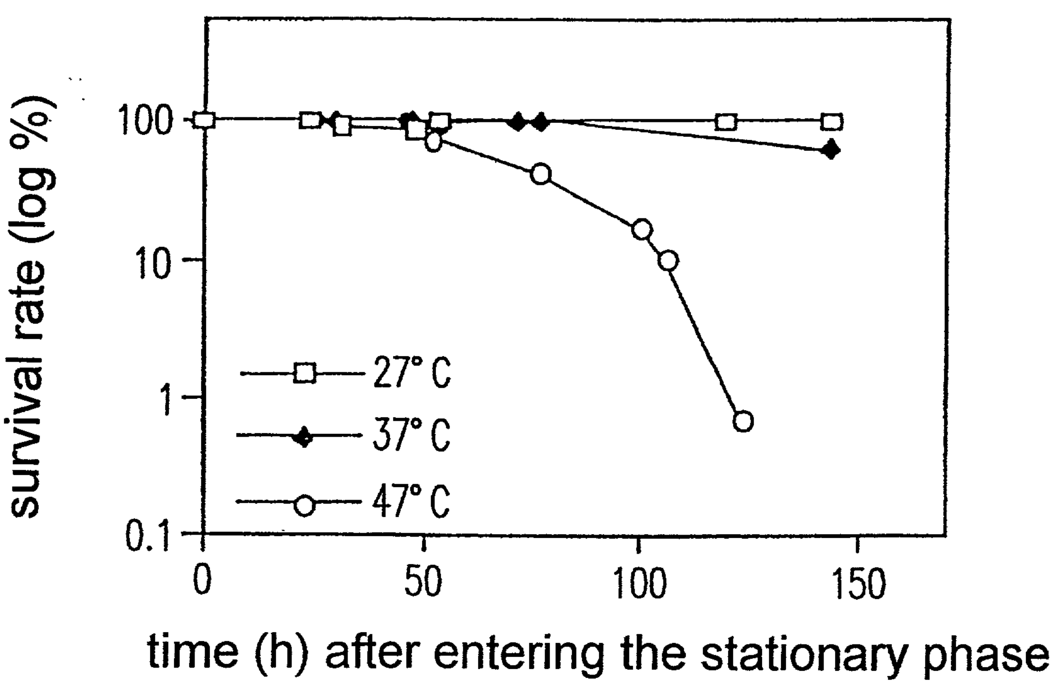

log OD (620 nm)
10
1
0.1
0
10
20
30
40
27° C
37° C
47° C
time (h) after inoculation

FIG. 2


survival rate (log %)
100
10
1
0.1
0
50
100
150
27° C
37° C
47° C
time (h) after entering the stationary phase

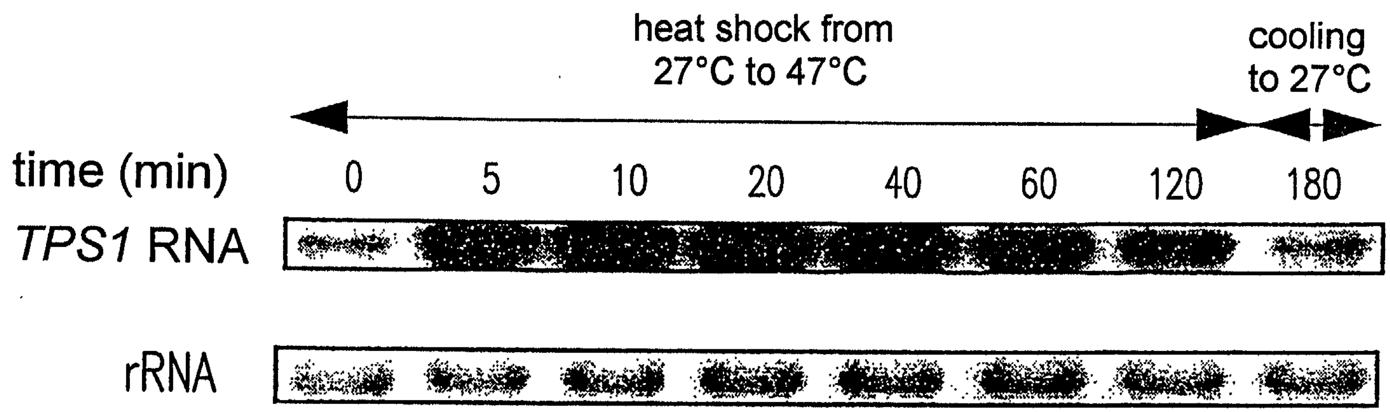

heat shock from
27°C to 47°C
cooling
to 27°C
time (min)
0
5
10
20
40
60
120
180
TPS1 RNA
rRNA

FIG. 3A

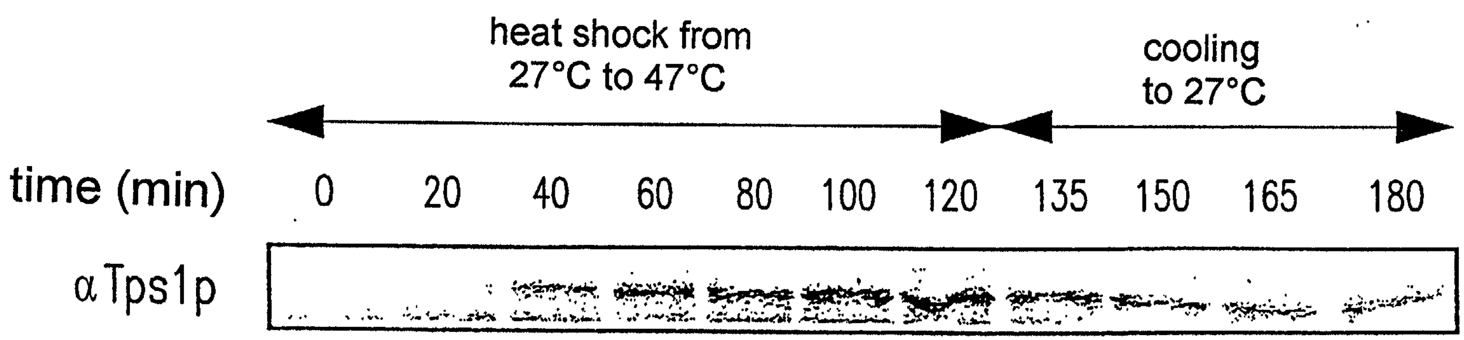

heat shock from
27°C to 47°C
cooling
to 27°C
time (min)
0
20
40
60
80
100
120
135
150
165
180
αTps1p

FIG. 3B

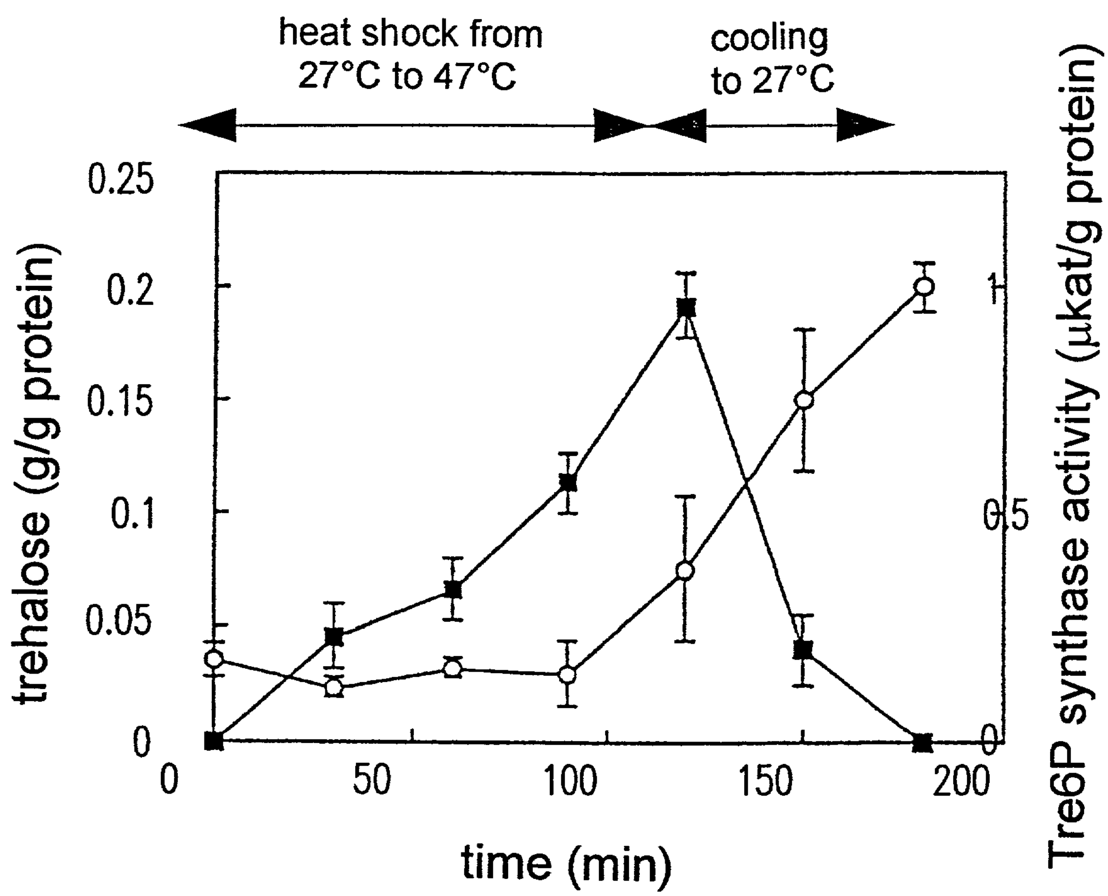

heat shock from
27°C to 47°C
cooling
to 27°C
0.25
0.2
0.15
0.1
0.05
0
trehalose (g/g protein)
0
50
100
150
200
time (min)
1
0.5
0
Tre6P synthase activity (µkat/g protein)

FIG. 3C

FIG. 4A

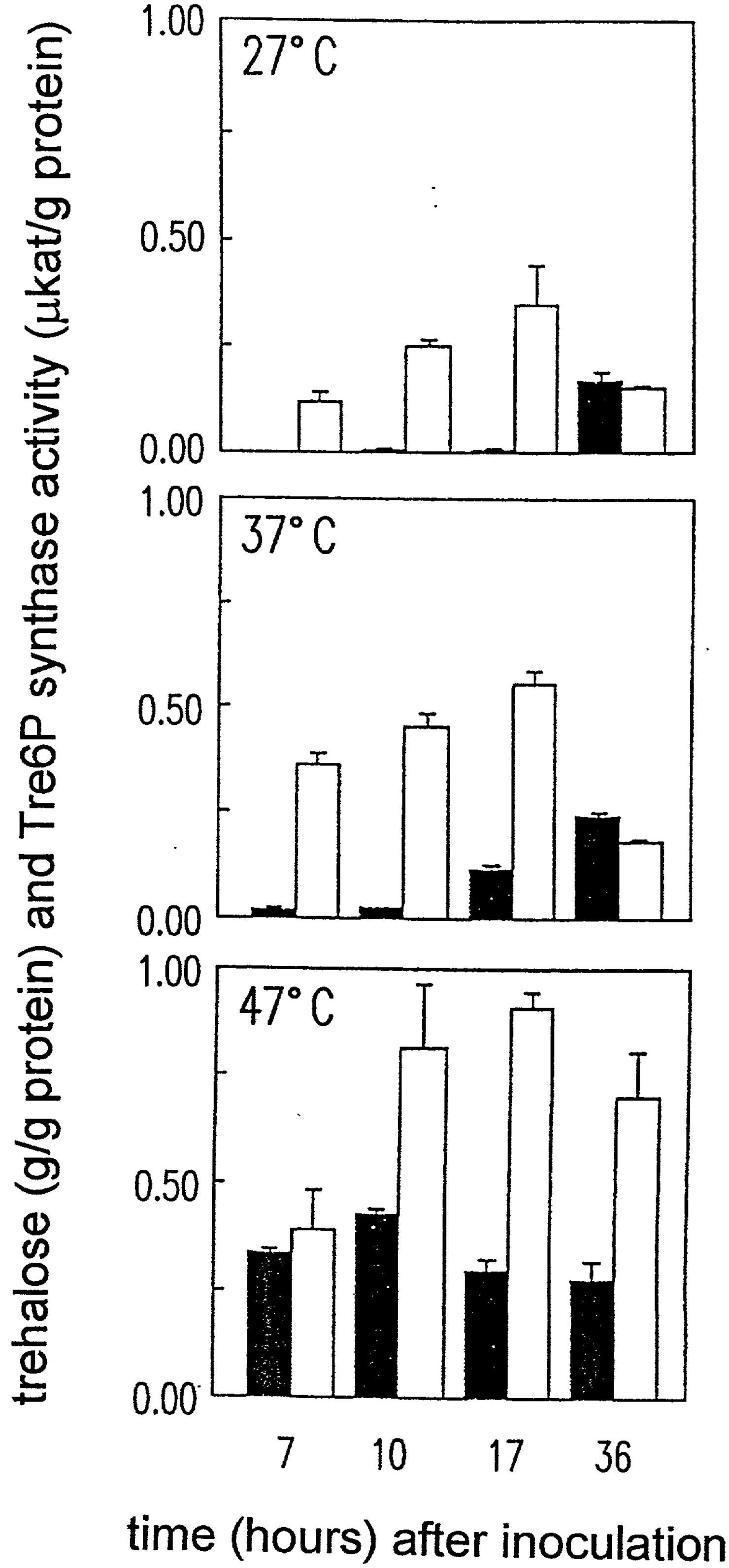

trehalose (g/g protein) and Tre6P synthase activity (µkat/g protein)
1.00
0.50
0.00
27° C
37° C
47° C
7
10
17
36
time (hours) after inoculation

FIG. 4B

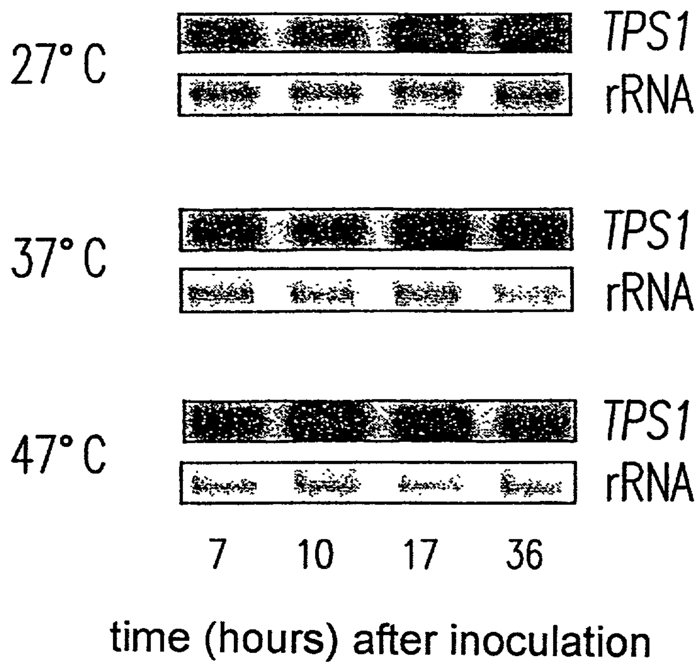
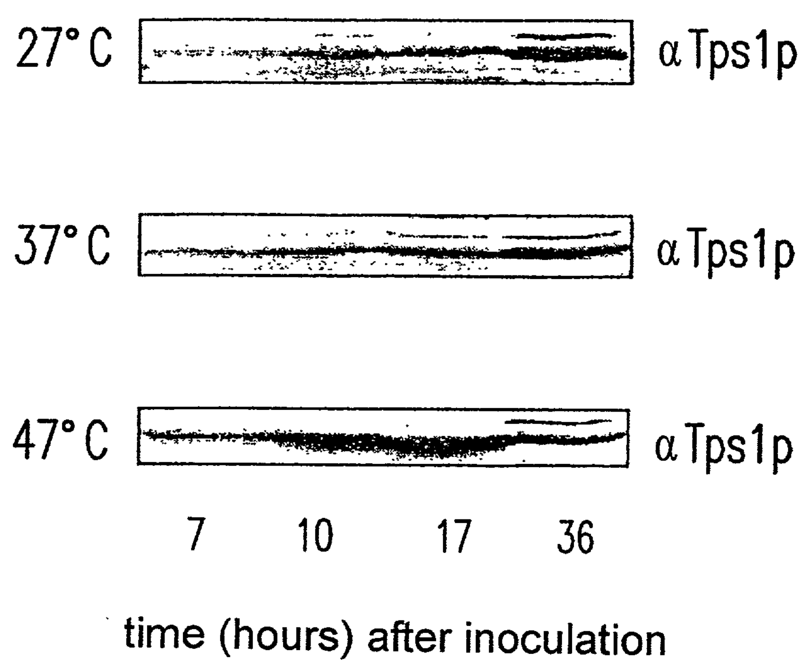

27° C
TPS1
rRNA
37° C
TPS1
rRNA
47° C
TPS1
rRNA
7
10
17
36
time (hours) after inoculation

FIG. 4C


27° C
αTps1p
37° C
αTps1p
47° C
αTps1p
7
10
17
36
time (hours) after inoculation

TPS1 from

	1001				1050
S. cerevisiae	AGCGATGAAA	TCGCAGACTT	AC.TCTACAA	CTGGTTCAGT	AATTCTATTC
K. lactis	AGTGACGAAG	TTGCTGATCT	TC.ATTACAA	CGGATTTTCC	AACTCTATTC
C. albicans	AGTGATACGA	TTGCTGATTT	AC.ATTATAA	TGGGTTTTCA	AATAGTATTT
S. pombe	GATGATGAGA	CTGCCGACCG	CC.ATTACAA	CGGATTTAGT	AACAGCATTC
A. niger	CTGAAGGCGC	TTGCTTGCTG	ACGGATATCC	ACTGCTCACA	GACTCCATTC

	1051				1100
S. cerevisiae	TATGGCCGTT	ATTCCATTAC	CATCCTGGTG	AGATCAATTT	CGACGAGAAT
K. lactis	TATGGCCATT	GTTCCATTAC	CATCCTGGTG	AGATCACTTT	CGATGACACT
C. albicans	TATGGCCACT	TTTCCATTAT	CATCCTGGGG	AAATGAACTT	TGATGAAAAT
S. pombe	TTTGGCCCTT	GTTCCACTAC	CATCCTGGTG	AAATTAATTT	TGACGAGGAA
A. niger	TCTGGCCCCT	CTTCCATTAC	CATCCCGGTG	AGATTACCTT	TGACGAGTCC

	1101				1150
S. cerevisiae	GCGTGGTAGG	CATACAACGA	GGCAAACCAG	ACGTTCACCA	ACGAGATTGC
K. lactis	GCATGGTTGG	CGTACAACGA	GGCAAATATG	GCTTTTGCCG	ATGAAATTGA
C. albicans	GAATGGGCAG	CATATATTGA	AGCCAATAAG	AAATTTGCAT	TGGAAATAGT
S. pombe	AATTGGGAGG	CCTATCGTGC	GGCTAACTAC	GCTTTTGCCG	AGGCCATTGT
A. niger	GCCTGGGAAG	CATACAAGGA	GGCCAACCGT	CTTTTCGCCA	AAGCGGTTGC

conserved regions

	1651				1700
S. cerevisiae	GTTGGTGTCG	ACAGG[illegible]	TTACATCAAA	GGTGTGCCTC	AGAAGTTGCA
K. lactis	ATTGGGGTCG	ATCGTCTTGA	TTACA[illegible]	GGTGTTCCTC	AGAAGTTACA
C. albicans	GTTGGTGTTG	ATAGATTAGA	CTATATCAAA	GGTGTTCCGC	AAAAATTACA
S. pombe	GTGGGTGTCG	ATCGTTTGGA	CTACATTAAG	GGTGTTCCCC	AAAAATTCCA
A. niger	GTGGGTGTGG	ACCGCCTGGA	TTACATCAAA	GGTGTCCCCC	AGAAGTTACA

	1701				1750
S. cerevisiae	CGCCATGGAA	GTGTTTCTGA	ACGAGCATCC	AGAATGGAGG	GGCAAGGTTG
K. lactis	CGCCTTGGAA	GTGTTCCTCG	GTGCGCATCC	TGAATGGATT	GGTAAGGTGG
C. albicans	TGCATTTGAA	GTCTTTTTGA	ATGAAAATCC	CGAATGGATT	GGCAAAGTAG
S. pombe	TGCCTTTGAA	GTGTTCTTAG	AACAATACCC	TGAATGGGTT	GGAAAGGTCG
A. niger	TGCCCTTGAG	GTGTTCCTTA	GCGATCATCC	GGAGTGGGTT	GGCAAGGTTG

FIG. 5

FIGUR 6

SEQ ID NO:8 (nucleic acid sequence)
SEQ ID NO:7 (amino acid sequence)

```
-792  CTTAAATACCACAATAGGAAAATTATCAATAAAGCTTTTCGGATTTCATTACGTTATATC -733
-732  GCAAAAAAATAGTCGAGCTTTCTGAACCGTTCGTTAATAAAAAAATAGTTTTTTCAGATT -673
-672  TCTATGTGAGGCAGTCACGATAGAATTCCATCGAACTCGTCAGCGCCAAATGTGAATGCG -613
-612  GCTTTCAAAAGCTTTGTCGAATTTGGGATGGGAATCCATGAATCGAAGATGTCAAAATGG -553
-552  GGGATCACAAAAGTACACTCACGAGGAAAATCAAAACCTTCTCGTACCTTTAACACATAC -493
-492  GGAAATGATCGATCGATTTGAGAAGATTCCTCAATGATTTTCGTCATATATAGGTATCTG -433
-432  AGGTATTTATGGACCGATTCGTAATAACATCATATACATCGCGCTTTGTCCCTGTCCCAG -373
-372  AGATTTCGATGAAAAAAGCGAATTTTATTCTAATATTTGAAGCATGCCAAACATGGGGCA -313
-312  GTTGATTTGTGTGAGGGTAAAATATCATGAATTGCACCCATCAAATGCAGCAAGATATTG -253
-252  ACCAATCCTATAATAGAAAACAGACTTACCACAAATAGATTGTGATGACGATATTATGAA -193
-192  TCTCCAGATGAAAGGCTCGAAAGCTATGAAGCCTCTTGAAACTTTTCATGGTGAGATAAT -133
-132  ATTTTCGAAATTTCCACGAACTTCTAAAACGCAATTATTGAATATAAAGGAAAAATAATA -73
 -72  TTTCCATATAGCAAGCAAATCAAGCTGCACTCCTCATCCTTAAAACTAATAAATCTTACC -13
 -12  CATTTGATACCAATGGTCAAAGGTAATGTTATAGTGGTTTCAAATAGAATCCCAGTCACT 48
   1              MetValLysGlyAsnValIleValValSerAsnArgIleProValThr 16

  49  ATTAAGAAGACTGAAGATGATGAAAATGGAAAATCAAGATACGACTATACAATGTCATCA 108
  17  IleLysLysThrGluAspAspGluAsnGlyLysSerArgTyrAspTyrThrMetSerSer 36

 109  GGCGGATTAGTGACGGCATTACAAGGGCTCAAAAATCCATTTCGATGGTTTGGATGGCCT 168
  37  GlyGlyLeuValThrAlaLeuGlnGlyLeuLysAsnProPheArgTrpPheGlyTrpPro 56

 169  GGGATGTCTGTTGATAGCGAACAGGGACGACAAACTGTCGAGCGGGATTTGAAGGAAAAG 228
  57  GlyMetSerValAspSerGluGlnGlyArgGlnThrValGluArgAspLeuLysGluLys 76

 229  TTCAATTGTTATCCGATATGGTTAAGTGACGAAATTGCAGACTTACATTATAACGGCTTT 288
  77  PheAsnCysTyrProIleTrpLeuSerAspGluIleAlaAspLeuHisTyrAsnGlyPhe 96

 289  AGCAATTCTATACTTTGGCCATTGTTCCACTATCACCCAGGGGAGATGAATTTTGATGAA 348
  97  SerAsnSerIleLeuTrpProLeuPheHisTyrHisProGlyGluMetAsnPheAspGlu 116

 349  ATTGCTTGGGCCGCTTATTTGGAAGCAAATAAACTGTTTTGCCAAACGATCTTAAAGGAG 408
 117  IleAlaTrpAlaAlaTyrLeuGluAlaAsnLysLeuPheCysGlnThrIleLeuLysGlu 136

 409  ATAAAAGACGGGGACGTTATCTGGGTACATGATTATCATCTCATGTTGTTGCCTTCACTG 468
 137  IleLysAspGlyAspValIleTrpValHisAspTyrHisLeuMetLeuLeuProSerLeu 156

 469  CTAAGAGACCAACTTAATAGTAAGGGGCTACCGAATGTCAAAATTGGCTTTTTCCTTCAT 528
 157  LeuArgAspGlnLeuAsnSerLysGlyLeuProAsnValLysIleGlyPhePheLeuHis 176

 529  ACTCCTTTTCCTTCAAGCGAAATATACAGGATACTTCCTGTAAGGAAAGAAATTCTCGAA 588
 177  ThrProPheProSerSerGluIleTyrArgIleLeuProValArgLysGluIleLeuGlu 196

 589  GGAGTGCTTAGTTGTGATTTGATAGGTTTCCACACCTATGATTATGTCCGTCACTTTCTT 648
 197  GlyValLeuSerCysAspLeuIleGlyPheHisThrTyrAspTyrValArgHisPheLeu 216

 649  AGTTCGGTTGAAAGAATATTGAAATTGCGAACGAGCCCACAAGGTGTTGTCTATAATGAT 708
 217  SerSerValGluArgIleLeuLysLeuArgThrSerProGlnGlyValValTyrAsnAsp 236
```

FIGUR 6

(cont.)

```
709  AGACAGGTGACTGTAAGTGCTTATCCGATTGGCATTGACGTTGACAAATTCTTGAATGGT  768
237  ArgGlnValThrValSerAlaTyrProIleGlyIleAspValAspLysPheLeuAsnGly  256

769  CTTAAGACTGATGAGGTCAAAAGCAGGATAAAACAGCTGGAAACCAGATTTGGTAAAGAT  828
257  LeuLysThrAspGluValLysSerArgIleLysGlnLeuGluThrArgPheGlyLysAsp  276

829  TGTAAACTTATTATTGGGGTGGACAGGCTGGATTACATCAAAGGTGTACCTCAAAAACTC  888
277  CysLysLeuIleIleGlyValAspArgLeuAspTyrIleLysGlyValProGlnLysLeu  296

889  CACGCGTTTGAAATTTTCTTGGAGAGACACCCTGAGTGGATTGGAAAAGTTGTTTTGATA  948
297  HisAlaPheGluIlePheLeuGluArgHisProGluTrpIleGlyLysValValLeuIle  316

949  CAGGTGGCTGTCCCCTCACGAGGGGACGTTGAAGAATATCAATCTTTGAGGGCAGCTGTA  1008
317  GlnValAlaValProSerArgGlyAspValGluGluTyrGlnSerLeuArgAlaAlaVal  336

1009 AATGAGCTAGTGGGAAGAATCAATGGTAGATTTGGTACCGTCGAATTTGTTCCTATCCAT  1068
337  AsnGluLeuValGlyArgIleAsnGlyArgPheGlyThrValGluPheValProIleHis  356

1069 TTCCTTCATAAAAGCGTGAACTTCCAAGAGCTGATATCTGTCTACGCTGCTAGTGATGTT  1128
357  PheLeuHisLysSerValAsnPheGlnGluLeuIleSerValTyrAlaAlaSerAspVal  376

1129 TGTGTAGTGTCATCGACACGGGACGGAATGAATTTGGTCAGTTATGAATACATTGCTTGT  1188
377  CysValValSerSerThrArgAspGlyMetAsnLeuValSerTyrGluTyrIleAlaCys  396

1189 CAACAAGATCGAAAGGGATCTCTAGTACTAAGTGAATTTGCGGGAGCTGCTCAGTCATTA  1248
397  GlnGlnAspArgLysGlySerLeuValLeuSerGluPheAlaGlyAlaAlaGlnSerLeu  416

1249 AATGGCGCTCTCGTAGTGAATCCATGGAATACAGAAGAACTCAGTGAAGCTATTTACGAA  1308
417  AsnGlyAlaLeuValValAsnProTrpAsnThrGluGluLeuSerGluAlaIleTyrGlu  436

1309 GGCTTGATCATGAGTGAAGAGAAAAGGAGGGGCAATTTTCAGAAGATGTTCAAGTACATT  1368
437  GlyLeuIleMetSerGluGluLysArgArgGlyAsnPheGlnLysMetPheLysTyrIle  456

1369 GAGAAATATACTGCAAGTTATTGGGGAGAGAACTTTGTGAAAGAATTGACGAGAGTGTGA  1428
457  GluLysTyrThrAlaSerTyrTrpGlyGluAsnPheValLysGluLeuThrArgVal    476

1429 TTACTGTGGTTTGCAGGTTAATTTGAAATGTTCACTTGTACTTGAAGAATTTTATATTAT  1488
1489 ATACATGTTATACATCAATAGGATAAAAATTAAGTAGACAAAGTTATCATTTTGTTGGGC  1548
1549 TGTAAAAATTGAACGATAACAATATATTTGACAAAATTAATTTGATCTAATTGAGCTGGA  1608
1609 GGGCGTAATATATTTGGTTTCCTGAATCATCTTGTAGATCACAATATGGGGCAGCTTCTT  1668
1669 TCGCAGCCGATCACAGAGAAACACATCACACTTGTCCAACATGATCACATATCGCATTCA  1728
1729 ATCGGGGAAATGCAAGGATACAGGTTGACCATGGAAGACGCGTTCTGTGATTTGAACGAA  1788
1789 AGAATATTCGTGACGGAAGAGGGACTTGACATCAGAAAACAAGACGAGAATACAGAGGGT  1848
1849 GATCTGGAGTCTCTTCAAATTAACATTTATGGTGTCTTTGACGGACATGGCGGTT       1903
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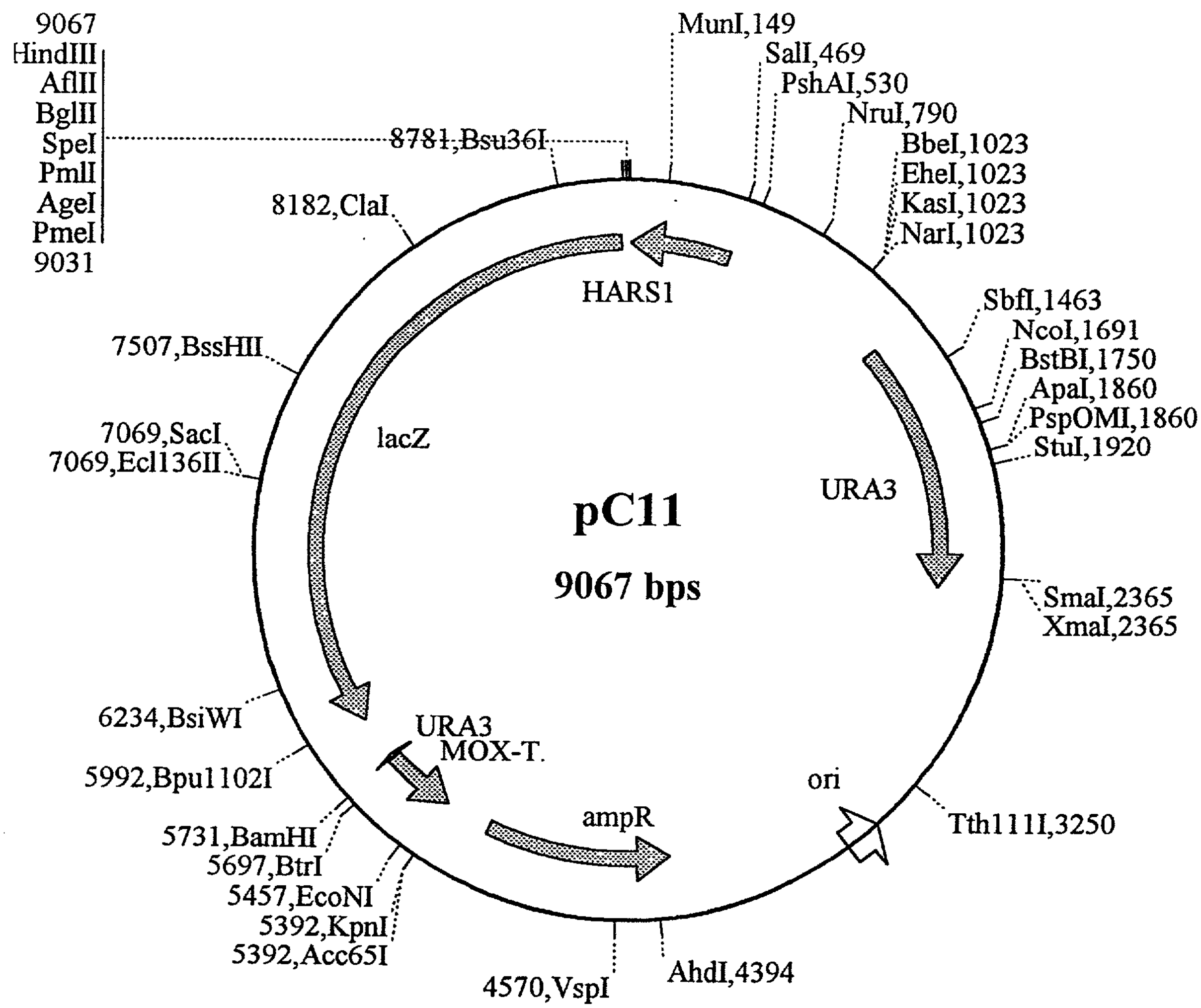

9067
HindIII
AflII
BglII
SpeI
PmlI
AgeI
PmeI
9031
8781,Bsu36I
MunI,149
SalI,469
PshAI,530
NruI,790
BbeI,1023
EheI,1023
KasI,1023
NarI,1023
8182,ClaI
HARS1
SbfI,1463
NcoI,1691
BstBI,1750
ApaI,1860
PspOMI,1860
StuI,1920
7507,BssHII
7069,SacI
7069,Ecl136II
lacZ
URA3
pC11
9067 bps
SmaI,2365
XmaI,2365
6234,BsiWI
URA3
MOX-T.
5992,Bpu1102I
ori
Tth111I,3250
ampR
5731,BamHI
5697,BtrI
5457,EcoNI
5392,KpnI
5392,Acc65I
4570,VspI
AhdI,4394

FIG. 7

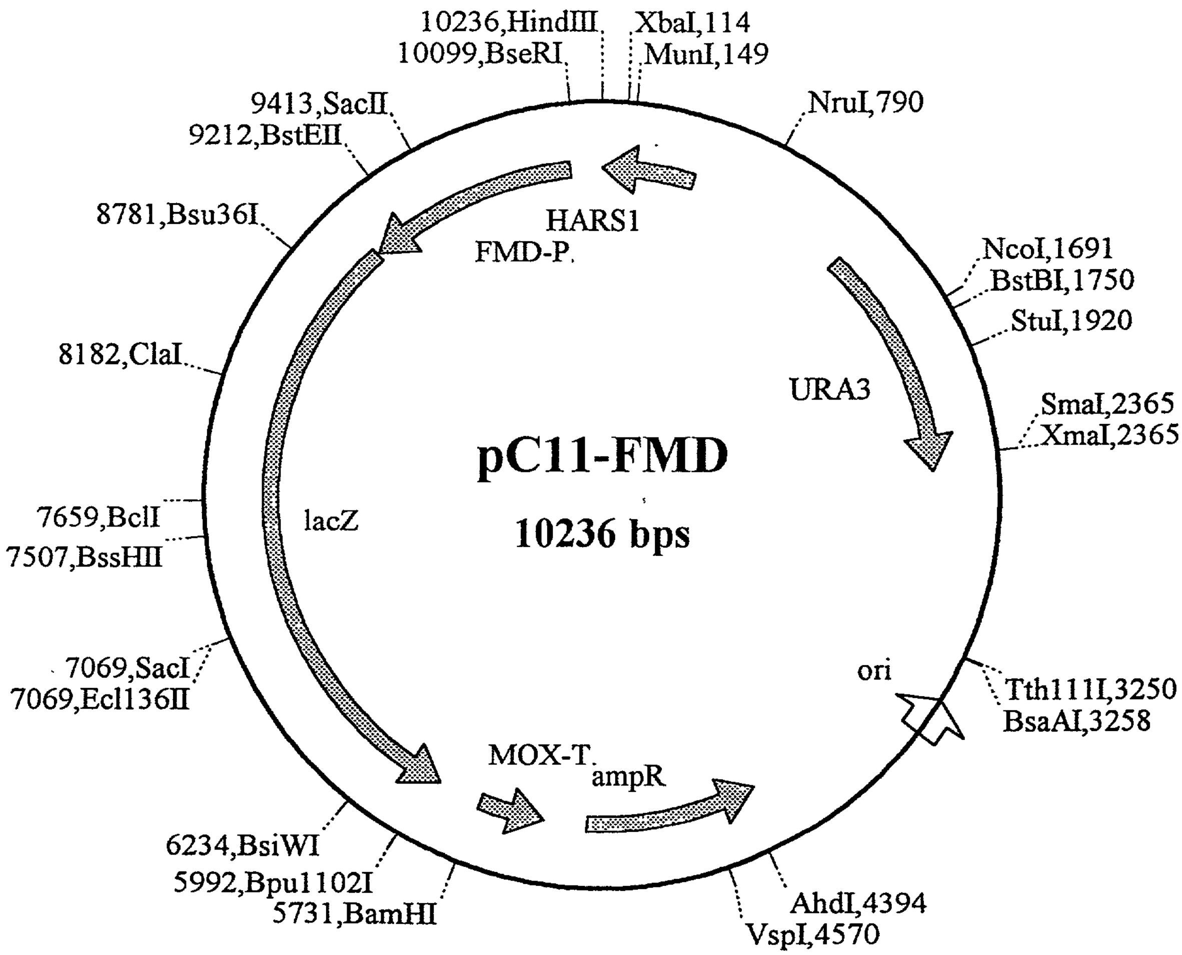

10236,HindIII
XbaI,114
10099,BseRI
MunI,149
9413,SacII
NruI,790
9212,BstEII
HARS1
8781,Bsu36I
FMD-P.
NcoI,1691
BstBI,1750
StuI,1920
8182,ClaI
URA3
SmaI,2365
XmaI,2365
pC11-FMD
10236 bps
7659,BclI
lacZ
7507,BssHII
7069,SacI
7069,Ecl136II
ori
Tth111I,3250
BsaAI,3258
MOX-T.
ampR
6234,BsiWI
5992,Bpu1102I
5731,BamHI
AhdI,4394
VspI,4570

FIG. 8

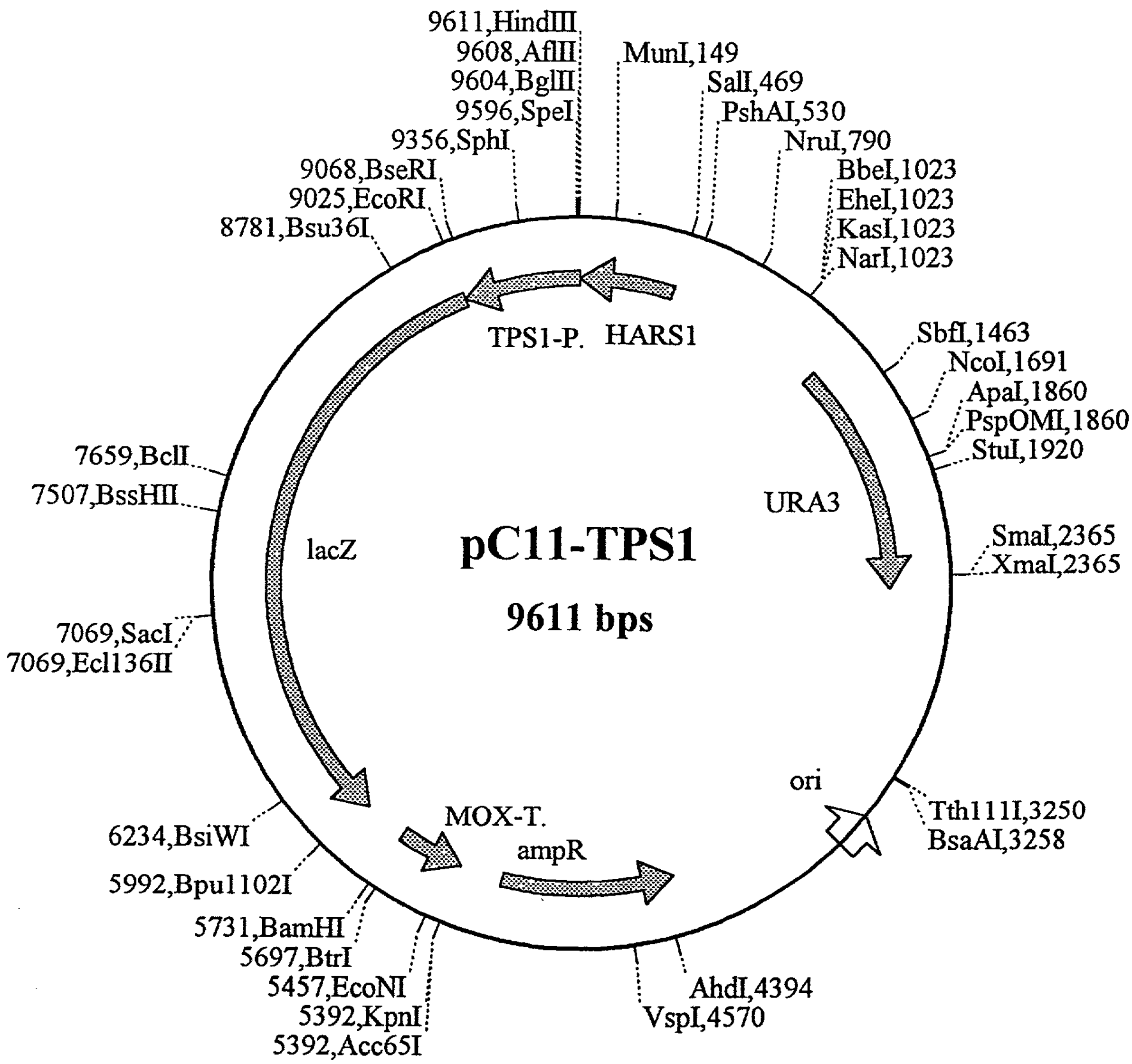

9611,HindIII
9608,AflII
9604,BglII
9596,SpeI
9356,SphI
9068,BseRI
9025,EcoRI
8781,Bsu36I
MunI,149
SalI,469
PshAI,530
NruI,790
BbeI,1023
EheI,1023
KasI,1023
NarI,1023
SbfI,1463
NcoI,1691
ApaI,1860
PspOMI,1860
StuI,1920
SmaI,2365
XmaI,2365
Tth111I,3250
BsaAI,3258
AhdI,4394
VspI,4570
5392,Acc65I
5392,KpnI
5457,EcoNI
5697,BtrI
5731,BamHI
5992,Bpu1102I
6234,BsiWI
7069,Ecl136II
7069,SacI
7507,BssHII
7659,BclI
TPS1-P.
HARS1
URA3
lacZ
pC11-TPS1
9611 bps
ori
MOX-T.
ampR

FIG. 9

FIG. 10A

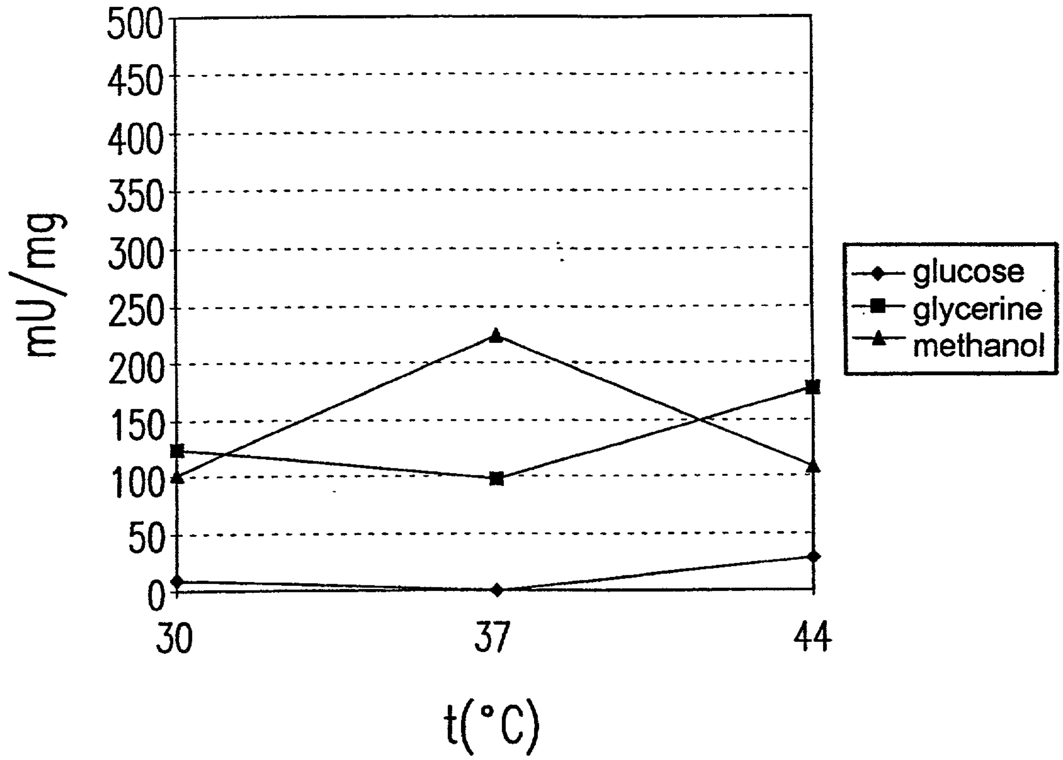
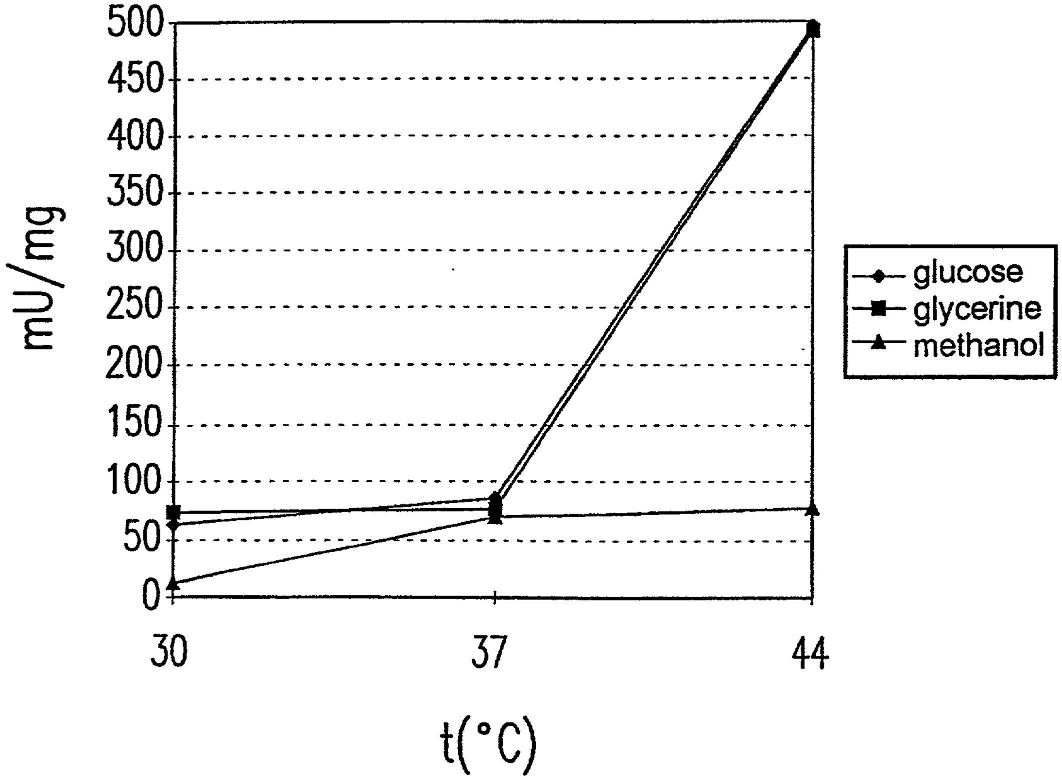


FIG. 10B



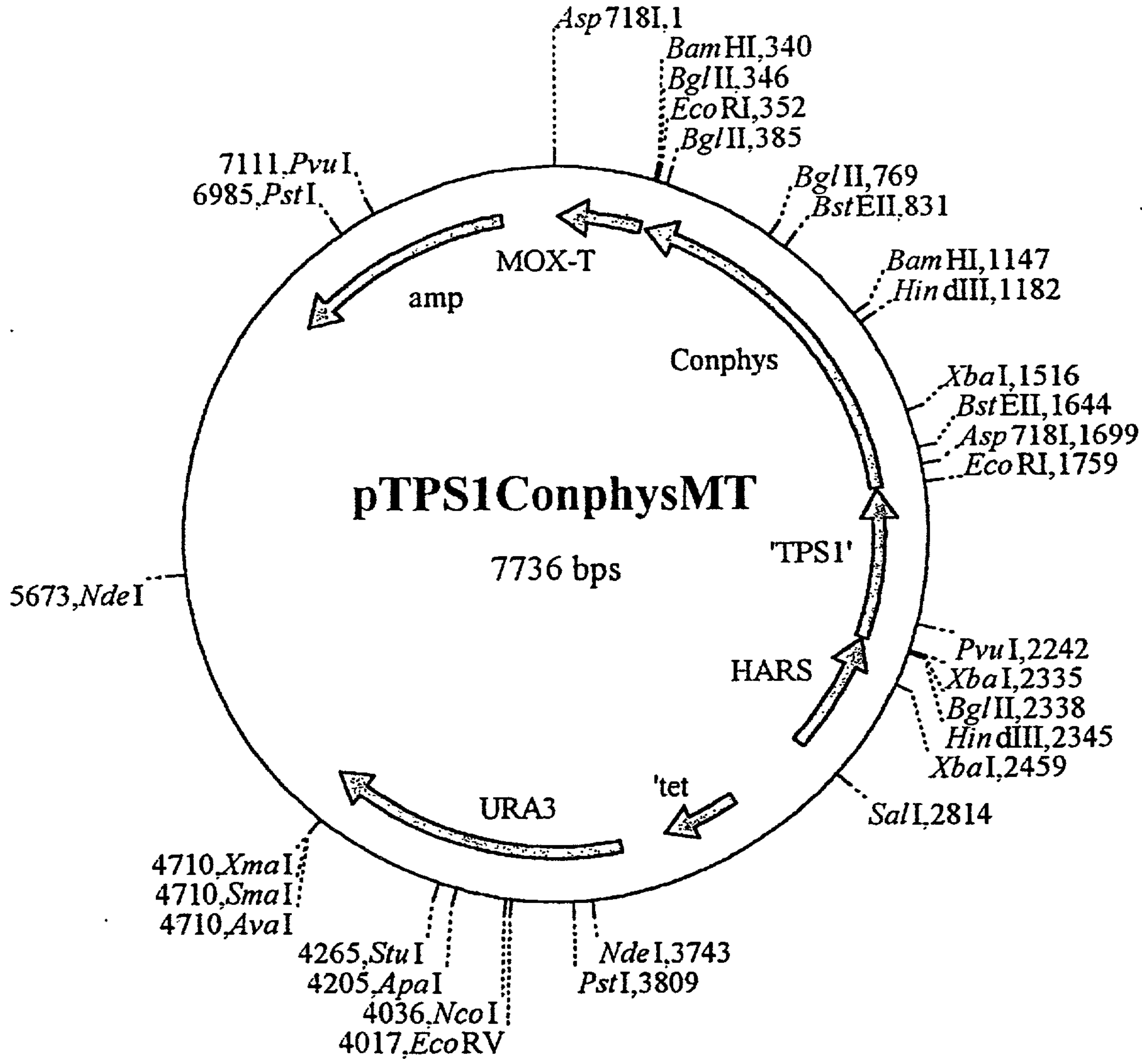

Asp718I,1
BamHI,340
BglII,346
EcoRI,352
BglII,385
BglII,769
BstEII,831
BamHI,1147
HindIII,1182
XbaI,1516
BstEII,1644
Asp718I,1699
EcoRI,1759
PvuI,2242
XbaI,2335
BglII,2338
HindIII,2345
XbaI,2459
SalI,2814
NdeI,3743
PstI,3809
4017,EcoRV
4036,NcoI
4205,ApaI
4265,StuI
4710,XmaI
4710,SmaI
4710,AvaI
5673,NdeI
6985,PstI
7111,PvuI
MOX-T
amp
Conphys
'TPS1'
HARS
'tet
URA3
pTPS1ConphysMT
7736 bps

FIG. 11